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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/935,061

DATE: 03/17/2003

TIME: 14:37:27

Input Set : D:\Seqlist.txt

Output Set: N:\CRF4\03172003\I935061.raw

3 <110> APPLICANT: Kobilka, Brian M.
4 Ghanouni, Pejman
5 Lee, Tae Weon
7 <120> TITLE OF INVENTION: Conformational assays to detect binding
8 to G protein-coupled receptors
11 <130> FILE REFERENCE: STAN213
13 <140> CURRENT APPLICATION NUMBER: 09/935,061
14 <141> CURRENT FILING DATE: 2001-08-21
16 <150> PRIOR APPLICATION NUMBER: 60/286,250
17 <151> PRIOR FILING DATE: 2001-04-24
19 <160> NUMBER OF SEQ ID NOS: 16
21 <170> SOFTWARE: FastSEQ for Windows Version 4.0
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 8
25 <212> TYPE: PRT
26 <213> ORGANISM: Artificial Sequence
28 <220> FEATURE:
29 <223> OTHER INFORMATION: epitope tag peptide
31 <400> SEQUENCE: 1
32 Asp Tyr Lys Asp Asp Asp Asp Lys
33 1 5
35 <210> SEQ ID NO: 2
36 <211> LENGTH: 8
37 <212> TYPE: PRT
38 <213> ORGANISM: Artificial Sequence
40 <220> FEATURE:
41 <223> OTHER INFORMATION: epitope tag peptide
43 <400> SEQUENCE: 2
44 Asp Tyr Lys Asp Glu Asp Asp Lys
45 1 5
47 <210> SEQ ID NO: 3
48 <211> LENGTH: 9
49 <212> TYPE: PRT
50 <213> ORGANISM: Artificial Sequence
52 <220> FEATURE:
53 <223> OTHER INFORMATION: epitope tag peptide
55 <400> SEQUENCE: 3
56 Ala Trp Arg His Pro Gln Phe Gly Gly
57 1 5
59 <210> SEQ ID NO: 4
60 <211> LENGTH: 13
61 <212> TYPE: PRT
62 <213> ORGANISM: Artificial Sequence

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64 <220> FEATURE:
65 <223> OTHER INFORMATION: epitope tag peptide
67 <400> SEQUENCE: 4
68 Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ile Glu Gly Arg
69 1 5 10
71 <210> SEQ ID NO: 5
72 <211> LENGTH: 1239
73 <212> TYPE: DNA
74 <213> ORGANISM: Homo sapiens
76 <220> FEATURE:
77 <221> NAME/KEY: CDS
78 <222> LOCATION: (1)...(1239)
80 <400> SEQUENCE: 5
81 atg ggg caa ccc ggg aac ggc agc gcc ttc ttg ctg gca ccc aat aga 48
82 Met Gly Gln Pro Gly Asn Gly Ser Ala Phe Leu Leu Ala Pro Asn Arg
83 1 5 10 15
85 agc cat gcg ccg gac cac gac gtc acg cag caa agg gac gag gtg tgg 96
86 Ser His Ala Pro Asp His Asp Val Thr Gln Gln Arg Asp Glu Val Trp
87 20 25 30
89 gtg gtg ggc atg ggc atc gtc atg tct ctc atc gtc ctg gcc atc gtg 144
90 Val Val Gly Met Gly Ile Val Met Ser Leu Ile Val Leu Ala Ile Val
91 35 40 45
93 ttt ggc aat gtg ctg gtc atc aca gcc att gcc aag ttc gag cgt ctg 192
94 Phe Gly Asn Val Leu Val Ile Thr Ala Ile Ala Lys Phe Glu Arg Leu
95 50 55 60
97 cag acg gtc acc aac tac ttc atc act tca ctg gcc tgt gct gat ctg 240
98 Gln Thr Val Thr Asn Tyr Phe Ile Thr Ser Leu Ala Cys Ala Asp Leu
99 65 70 75 80
101 gtc atg ggc ctg gca gtg gtg ccc ttt ggg gcc gcc cat att ctt atg 288
102 Val Met Gly Leu Ala Val Val Pro Phe Gly Ala Ala His Ile Leu Met
103 85 90 95
105 aaa atg tgg act ttt ggc aac ttc tgg tgc gag ttt tgg act tcc att 336
106 Lys Met Trp Thr Phe Gly Asn Phe Trp Cys Glu Phe Trp Thr Ser Ile
107 100 105 110
109 gat gtg ctg tgc gtc acg gct agc att gag acc ctg tgc gtg atc gca 384
110 Asp Val Leu Cys Val Thr Ala Ser Ile Glu Thr Leu Cys Val Ile Ala
111 115 120 125
113 gtg gat cgc tac ttt gcc att act tca cct ttc aag tac cag agc ctg 432
114 Val Asp Arg Tyr Phe Ala Ile Thr Ser Pro Phe Lys Tyr Gln Ser Leu
115 130 135 140
117 ctg acc aag aat aag gcc cgg gtg atc att ctg atg gtg tgg att gtg 480
118 Leu Thr Lys Asn Lys Ala Arg Val Ile Ile Leu Met Val Trp Ile Val
119 145 150 155 160
121 tca ggc ctt acc tcc ttc ttg ccc att cag atg cac tgg tac cgg gcc 528
122 Ser Gly Leu Thr Ser Phe Leu Pro Ile Gln Met His Trp Tyr Arg Ala
123 165 170 175
125 acc cac cag gaa gcc atc aac tgc tat gcc aat gag acc tgc tgt gac 576
126 Thr His Gln Glu Ala Ile Asn Cys Tyr Ala Asn Glu Thr Cys Cys Asp
127 180 185 190

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129 ttc ttc acg aac caa gcc tat gcc att gcc tct tcc atc gtg tcc ttc      624
130 Phe Phe Thr Asn Gln Ala Tyr Ala Ile Ala Ser Ser Ile Val Ser Phe
131      195      200      205
133 tac gtt ccc ctg gtg atc atg gtc ttc gtc tac tcc agg gtc ttt cag      672
134 Tyr Val Pro Leu Val Ile Met Val Phe Val Tyr Ser Arg Val Phe Gln
135      210      215      220
137 gag gcc aaa agg cag ctc cag aag att gac aaa tct gag ggc cgc ttc      720
138 Glu Ala Lys Arg Gln Leu Gln Lys Ile Asp Lys Ser Glu Gly Arg Phe
139 225      230      235      240
141 cat gtc cag aac ctt agc cag gtg gag cag gat ggg cgg acg ggg cat      768
142 His Val Gln Asn Leu Ser Gln Val Glu Gln Asp Gly Arg Thr Gly His
143      245      250      255
145 gga ctc cgc aga tct tcc aag ttc tgc ttg aag gag cac aaa gcc ctc      816
146 Gly Leu Arg Arg Ser Ser Lys Phe Cys Leu Lys Glu His Lys Ala Leu
147      260      265      270
149 aag acg tta ggc atc atc atg ggc act ttc acc ctc tgc tgg ctg ccc      864
150 Lys Thr Leu Gly Ile Ile Met Gly Thr Phe Thr Leu Cys Trp Leu Pro
151      275      280      285
153 ttc ttc atc gtt aac att gtg cat gtg atc cag gat aac ctc atc cgt      912
154 Phe Phe Ile Val Asn Ile Val His Val Ile Gln Asp Asn Leu Ile Arg
155      290      295      300
157 aag gaa gtt tac atc ctc cta aat tgg ata ggc tat gtc aat tct ggt      960
158 Lys Glu Val Tyr Ile Leu Leu Asn Trp Ile Gly Tyr Val Asn Ser Gly
159 305      310      315      320
161 ttc aat ccc ctt atc tac tgc cgg agc cca gat ttc agg att gcc ttc      1008
162 Phe Asn Pro Leu Ile Tyr Cys Arg Ser Pro Asp Phe Arg Ile Ala Phe
163      325      330      335
165 cag gag ctc ctg tgc ctg cgc agg tct tct ttg aag gcc tat ggg aat      1056
166 Gln Glu Leu Leu Cys Leu Arg Arg Ser Ser Leu Lys Ala Tyr Gly Asn
167      340      345      350
169 ggc tac tcc agc aac ggc aac aca ggg gag cag agt gga tat cac gtg      1104
170 Gly Tyr Ser Ser Asn Gly Asn Thr Gly Glu Gln Ser Gly Tyr His Val
171      355      360      365
173 gaa cag gag aaa gaa aat aaa ctg ctg tgt gaa gac ctc cca ggc acg      1152
174 Glu Gln Glu Lys Glu Asn Lys Leu Leu Cys Glu Asp Leu Pro Gly Thr
175      370      375      380
177 gaa gac ttt gtg ggc cat caa ggt act gtg cct agc gat aac att gat      1200
178 Glu Asp Phe Val Gly His Gln Gly Thr Val Pro Ser Asp Asn Ile Asp
179 385      390      395      400
181 tca caa ggg agg aat tgt agt aca aat gac tca ctg ctg      1239
182 Ser Gln Gly Arg Asn Cys Ser Thr Asn Asp Ser Leu Leu
183      405      410
186 <210> SEQ ID NO: 6
187 <211> LENGTH: 413
188 <212> TYPE: PRT
189 <213> ORGANISM: Homo sapiens
191 <400> SEQUENCE: 6
192 Met Gly Gln Pro Gly Asn Gly Ser Ala Phe Leu Leu Ala Pro Asn Arg
193 1      5      10      15

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194 Ser His Ala Pro Asp His Asp Val Thr Gln Gln Arg Asp Glu Val Trp
195      20      25      30
196 Val Val Gly Met Gly Ile Val Met Ser Leu Ile Val Leu Ala Ile Val
197      35      40      45
198 Phe Gly Asn Val Leu Val Ile Thr Ala Ile Ala Lys Phe Glu Arg Leu
199      50      55      60
200 Gln Thr Val Thr Asn Tyr Phe Ile Thr Ser Leu Ala Cys Ala Asp Leu
201 65      70      75      80
202 Val Met Gly Leu Ala Val Val Pro Phe Gly Ala Ala His Ile Leu Met
203      85      90      95
204 Lys Met Trp Thr Phe Gly Asn Phe Trp Cys Glu Phe Trp Thr Ser Ile
205      100     105     110
206 Asp Val Leu Cys Val Thr Ala Ser Ile Glu Thr Leu Cys Val Ile Ala
207      115     120     125
208 Val Asp Arg Tyr Phe Ala Ile Thr Ser Pro Phe Lys Tyr Gln Ser Leu
209      130     135     140
210 Leu Thr Lys Asn Lys Ala Arg Val Ile Ile Leu Met Val Trp Ile Val
211 145     150     155     160
212 Ser Gly Leu Thr Ser Phe Leu Pro Ile Gln Met His Trp Tyr Arg Ala
213      165     170     175
214 Thr His Gln Glu Ala Ile Asn Cys Tyr Ala Asn Glu Thr Cys Cys Asp
215      180     185     190
216 Phe Phe Thr Asn Gln Ala Tyr Ala Ile Ala Ser Ser Ile Val Ser Phe
217      195     200     205
218 Tyr Val Pro Leu Val Ile Met Val Phe Val Tyr Ser Arg Val Phe Gln
219      210     215     220
220 Glu Ala Lys Arg Gln Leu Gln Lys Ile Asp Lys Ser Glu Gly Arg Phe
221 225     230     235     240
222 His Val Gln Asn Leu Ser Gln Val Glu Gln Asp Gly Arg Thr Gly His
223      245     250     255
224 Gly Leu Arg Arg Ser Ser Lys Phe Cys Leu Lys Glu His Lys Ala Leu
225      260     265     270
226 Lys Thr Leu Gly Ile Ile Met Gly Thr Phe Thr Leu Cys Trp Leu Pro
227      275     280     285
228 Phe Phe Ile Val Asn Ile Val His Val Ile Gln Asp Asn Leu Ile Arg
229      290     295     300
230 Lys Glu Val Tyr Ile Leu Leu Asn Trp Ile Gly Tyr Val Asn Ser Gly
231 305     310     315     320
232 Phe Asn Pro Leu Ile Tyr Cys Arg Ser Pro Asp Phe Arg Ile Ala Phe
233      325     330     335
234 Gln Glu Leu Leu Cys Leu Arg Arg Ser Ser Leu Lys Ala Tyr Gly Asn
235      340     345     350
236 Gly Tyr Ser Ser Asn Gly Asn Thr Gly Glu Gln Ser Gly Tyr His Val
237      355     360     365
238 Glu Gln Glu Lys Glu Asn Lys Leu Leu Cys Glu Asp Leu Pro Gly Thr
239      370     375     380
240 Glu Asp Phe Val Gly His Gln Gly Thr Val Pro Ser Asp Asn Ile Asp
241 385     390     395     400
242 Ser Gln Gly Arg Asn Cys Ser Thr Asn Asp Ser Leu Leu

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243                               405                               410
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246 <211> LENGTH: 1239
247 <212> TYPE: DNA
248 <213> ORGANISM: Artificial Sequence
250 <220> FEATURE:
251 <223> OTHER INFORMATION: Beta-2 Adrenergic Receptor with TEV site in 2nd
252     intracellular loop
W--> 254 <221> NAME/KEY: CDS
255 <222> LOCATION: (1)...(1239)
W--> 257 <400> 7
258 atg ggg caa ccc ggg aac ggc agc gcc ttc ttg ctg gca ccc aat aga      48
259 Met Gly Gln Pro Gly Asn Gly Ser Ala Phe Leu Leu Ala Pro Asn Arg
260 1      5      10      15
262 agc cat gcg ccg gac cac gac gtc acg cag caa agg gac gag gtg tgg      96
263 Ser His Ala Pro Asp His Asp Val Thr Gln Gln Arg Asp Glu Val Trp
264      20      25      30
266 gtg gtg ggc atg ggc atc gtc atg tct ctc atc gtc ctg gcc atc gtg      144
267 Val Val Gly Met Gly Ile Val Met Ser Leu Ile Val Leu Ala Ile Val
268      35      40      45
270 ttt ggc aat gtg ctg gtc atc aca gcc att gcc aag ttc gag cgt ctg      192
271 Phe Gly Asn Val Leu Val Ile Thr Ala Ile Ala Lys Phe Glu Arg Leu
272      50      55      60
274 cag acg gtc acc aac tac ttc atc act tca ctg gcc tgt gct gat ctg      240
275 Gln Thr Val Thr Asn Tyr Phe Ile Thr Ser Leu Ala Cys Ala Asp Leu
276 65      70      75      80
278 gtc atg ggc ctg gca gtg gtg ccc ttt ggg gcc gcc cat att ctt atg      288
279 Val Met Gly Leu Ala Val Val Pro Phe Gly Ala Ala His Ile Leu Met
280      85      90      95
282 aaa atg tgg act ttt ggc aac ttc tgg tgc gag ttt tgg act tcc att      336
283 Lys Met Trp Thr Phe Gly Asn Phe Trp Cys Glu Phe Trp Thr Ser Ile
284      100      105      110
286 gat gtg ctg tgc gtc acg gct agc att gag acc ctg tgc gtg atc gca      384
287 Asp Val Leu Cys Val Thr Ala Ser Ile Glu Thr Leu Cys Val Ile Ala
288      115      120      125
290 gtg gat cgc tac ttt gcc att act tca cct ttc aag tac cag agc ctg      432
291 Val Asp Arg Tyr Phe Ala Ile Thr Ser Pro Phe Lys Tyr Gln Ser Leu
292      130      135      140
294 ctg acc aag aat aag gcc cgg gtg atc att ctg atg gtg tgg att gtg      480
295 Leu Thr Lys Asn Lys Ala Arg Val Ile Ile Leu Met Val Trp Ile Val
296 145      150      155      160
298 tca ggc ctt acc tcc ttc ttg ccc att cag atg cac tgg tac cgg gcc      528
299 Ser Gly Leu Thr Ser Phe Leu Pro Ile Gln Met His Trp Tyr Arg Ala
300      165      170      175
302 acc cac cag gaa gcc atc aac tgc tat gcc aat gag acc tgc tgt gac      576
303 Thr His Gln Glu Ala Ile Asn Cys Tyr Ala Asn Glu Thr Cys Cys Asp
304      180      185      190
306 ttc ttc acg aac caa gcc tat gcc att gcc tct tcc atc gtg tcc ttc      624
307 Phe Phe Thr Asn Gln Ala Tyr Ala Ile Ala Ser Ser Ile Val Ser Phe

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VERIFICATION SUMMARY

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Input Set : D:\Seqlist.txt

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L:254 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:257 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:7
L:435 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:438 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:9
L:790 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:793 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:13
L:965 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:968 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:15